

Please amend the application as follows:

1. (previously presented) A method for identifying the phenotype[s] of increased rib eye area in s-in-cattle a *Bos taurus* animal, the method comprising:

isolating a nucleic acid sample from the animal; and

detecting a determining whether the animal has a T/C polymorphism present in the insulin-like growth factor 2 (*IGF2*) *IGF2* gene at position 150 of SEQ ID NO: 1; and

wherein the presence of a C residue (a C allele) at position 150 of SEQ ID NO : 1 is associated with the phenotype[s] of at least one of increased rib eye area, decreased fat content and decreased marbling, as compared to an animal cattle with a T residue (T allele) at position 150 of SEQ ID NO : 1.

2. (currently amended) The method of Claim 1 wherein detecting the polymorphism comprises:

isolating a genomic DNA sample from the animal;cattle;

amplifying a region of the *Bos taurus* bovine *IGF2* gene using an oligonucleotide pair to form nucleic acid amplification products comprising amplified *IGF2* gene polymorphism sequences;

analyzing the amplification products to determine the presence or absence of the at least one C allele at position 150 of SEQ ID NO : 1.

3. (original) The method of Claim 2 wherein the oligonucleotide pair comprises SEQ ID NO: 2 and SEQ ID NO: 3.
4. (previously presented) The method of Claim 3 wherein the polymorphism detected is step of analyzing the amplification products comprises assessing whether they have a restriction fragment length polymorphism (RFLP).

5. (original) The method of Claim 4 wherein the RFLP is the presence or absence of a *BsrI* restriction site at nucleotide 150 in a nucleic acid amplification product produced by amplification of a portion of the *IGF2* gene using the oligonucleotide pair SEQ ID NO: 2 and SEQ ID NO : 3.
6. (original) The method of Claim 2 further comprising the inclusion of a detectable moiety such that the amplification product comprises a labeled amplification product.
7. (original) The method of Claim 6 wherein the detectable moiety is selected from the group consisting of fluorescent, bioluminescent, chemiluminescent, radioactive and colorigenic moieties.
8. (previously presented) The method of Claim [4] [2] further comprising:  
  
contacting the nucleic acid amplification products with a hybridization probe;  
  
wherein the hybridization probes comprise at least one oligonucleotide labeled with a detectable moiety;  
  
under suitable conditions permitting hybridization of the at least one oligonucleotide to the amplification product[s] to form a hybridization complex;  
  
and  
  
wherein the presence of the detectable moiety in the hybridization complex indicates the presence of a *IGF2* polymorphism.
9. (previously presented) The method of Claim [4] [2] wherein the nucleic acid amplification products are is produced by an amplification method selected from the group of polymerase chain reaction (PCR), strand displacement amplification (SDA), nucleic acid sequence based amplification (NASBA), rolling circle amplification, T7 polymerase mediated amplification, T3 polymerase mediated amplification and SP6 polymerase mediated amplification.
10. (withdrawn) An isolated and purified nucleic acid comprising a portion of the bovine *IGF2* gene, further comprising a polymorphism at position 150 as defined

by the positions in SEQ ID NO: 1, and in which there is a C residue or a T residue at position 150.

11. (previously presented) A method of selecting sorting individual Bos taurus animals cattle-based on the knowledge of an the animal's insulin-like growth factor 2 (IGF2) IGF2 genotype, comprising the steps of:

determining whether the animal has C alleles or T alleles in the IGF2 gene at position 150 of SEQ ID NO: 1 the IGF2-alleles of an animal;

wherein the alleles genotype of an the animal are will be one of C/C, C/T ~~CT~~, or T/T with respect to detected at position 150 of SEQ ID NO : 1; and

sorting the animals into groups of like genotype; and

wherein a C/C or C/T ~~genotype~~ is associated with the phenotype of increased rib-eye area, decreased fat content, and marbling as compared to T/T cattle.

12. (withdrawn) A diagnostic kit for determining the IGF2 genotype at position 150 of sequence ID NO: 1 in the IGF2 gene of a bovine animal, the kit comprising:

oligonucleotide primers for amplifying a portion of the IGF2 gene;

the primers comprising a forward primer comprising, at it's 3' end, sequence identical to at least 10 contiguous nucleotides within SEQ ID NO: 1;

a reverse primer comprising, at it's 3' end, a nucleotide sequence fully complementary to at least 10 contiguous nucleotides with SEQ ID NO: 1;

and wherein the forward and reverse primers will produce, in a PCR amplification reaction, a nucleic acid product amplification product containing a residue corresponding to position 150 of SEQ ID NO : 1.

13. (withdrawn) The kit of Claim 12 wherein the primers comprise the oligonucleotides SEQ ID NO: 2 and SEQ ID NO: 3.

14. (withdrawn) The kit of Claim 12 wherein the primers are labeled with a detectable moiety.
15. (withdrawn) The kit of Claim 12 further comprising at least one oligonucleotide, labeled with a detectable moiety and suitable for use as a hybridization probe.
16. (cancelled) A method for identifying sires that will pass on a phenotype of lower birth weight to offspring, the method comprising:  
  
detecting a polymorphism in a sire present in the *IGF2* gene at position 150 of SEQ ID NO : 1;  
  
wherein the presence of a C residue at position 150 of SEQ ID NO: 1 in both *IGF2* gene alleles (a C/C sire) is associated with the phenotype of production of offspring with lower birth weight, as compared to sires with a T residue at position 150 of SEQ ID NO: 1 in both *IGF2* gene alleles (a T/T sire).
17. (cancelled) The method of Claim 16 wherein detecting the polymorphism comprises:  
  
isolating a genomic DNA sample from cattle;  
  
amplifying a region of the bovine *IGF2* gene using an oligonucleotide pair to form nucleic acid amplification products comprising amplified *IGF2* gene polymorphism sequences;  
  
analyzing the amplification products to determine the presence or absence of a C allele and a T allele.
18. (cancelled) A method of cattle production that reduces birth weight comprising breeding dams to sires having a C residue at position 150 of SEQ ID NO : 1 in both *IGF2* gene alleles (C/C sires).
19. (cancelled) A method of cattle production that increases birth weight comprising breeding dams to sires having a T residue at position 150 of SEQ ID NO: 1 in both *IGF2* gene alleles (T/T sires).

20. (currently amended) A method for genotyping a *Bos taurus* animal comprising:

isolating a genomic DNA sample from the animal;

determining whether the animal has C residue (a C allele) or T residue (a T allele) in the insulin-like growth factor 2 (*IGF 2*) gene at position 150 of SEQ ID NO : 1, and

assigning either the C/C, C/T or T/T genotype, at position 150 of SEQ ID NO : 1, to the animal, and

wherein the C/C or C/T genotype is associated with increased rib-eye area as compared to the T/T genotype.

21. (previously presented) The method of Claim 20 wherein the step of determining comprises amplifying a region of the *Bos taurus IGF 2* gene in the isolated genomic DNA sample, using an oligonucleotide pair, to form nucleic acid amplification products comprising position 150 of SEQ ID NO : 1, and analyzing the amplification products to determine whether they have a C residue (a C allele) or T residue (a T allele).

## REMARKS

### **35 USC § 112/Second Paragraph**

The Examiner objected to claims 2-7 on the basis that the use of the term "the at least one C allele" in claims 2-7 renders the claims unclear, because it is not clear if this is a reference to the C allele at position 150, or to another C allele in *IGF2*.

Claim 2 has been amended to add "at position 150 of SEQ ID NO : 1" to the end of the claim. Claims 3 to 7 depend from claim.

### **35 USC § 112/Written Description**

The Examiner has rejected claims 1-9 on the basis that the specification fails to comply with the written description requirement in respect of these claims. The Examiner contends that the description does not enable identification of the phenotype of increased rib eye area by detecting only the presence of a single C allele at position 150 of SEQ ID No: 1. The Applicant respectfully disagrees.

There are several statements in the application which clearly state that rib-eye area is determined by the number of C alleles, and therefore that the inventors knew that C/T animals had a smaller rib-eye area than C/C animals and a larger rib-eye area than T/T animals. For example:

In the 125 cattle studied, REA size was significantly correlated with **the number of C alleles** present in the population. ( $r=0.39$ ,  $P=0.0001$ ) (page 34, 2<sup>nd</sup> paragraph)

The effect on REA is significantly correlated with **the number of C alleles** suggesting a **co-dominant** inheritance pattern. (page 35, 2<sup>nd</sup> paragraph)

The SNP-2 genotype also affects REA size, such that animals with a C residue at the SNP-2 site in both *IGF2* alleles (C/C offspring) will display **the greater increase** in REA size. (page 11, 2<sup>nd</sup> paragraph)